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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/000,151B

DATE: 08/12/2002

TIME: 09:42:25

Input Set : A:\HERG-KCR1rev1.ST25.txt
 Output Set: N:\CRF4\08122002\J000151B.raw

3 <110> APPLICANT: Balser, Jeffrey R.
 4 George, Alfred L.
 6 <120> TITLE OF INVENTION: HUMAN KCR1 REGULATION OF HERG POTASSIUM CHANNEL BLOCK
 8 <130> FILE REFERENCE: Vanderbilt Ref No. VU0120; Attorney Docket No. 1242-49
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/000,151B
 11 <141> CURRENT FILING DATE: 2000-10-30
 13 <160> NUMBER OF SEQ ID NOS: 5
 15 <170> SOFTWARE: PatentIn version 3.1
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 1857
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Homo sapiens
 22 <220> FEATURE:
 23 <221> NAME/KEY: misc_feature
 24 <222> LOCATION: (1)..(1857)
 25 <223> OTHER INFORMATION: n is any nucleic acid
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (1)..(1422)
 31 <223> OTHER INFORMATION: n is any nucleic acid
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 37 1 5 10 15
 39 ttt tta gtg tcc tgc ctc ctc ttc tcc gcc ttc agc cgg gcg ctg cga 96
 40 Phe Leu Val Ser Cys Leu Leu Phe Ser Ala Phe Ser Arg Ala Leu Arg
 41 20 25 30
 43 gag ccc tac atg gac gag atc ttc cac ctg cct cag gcg cag cgc tac 144
 44 Glu Pro Tyr Met Asp Glu Ile Phe His Leu Pro Gln Ala Gln Arg Tyr
 45 35 40 45
 47 tgt gag ggc cat ttc tcc ctt tcc cag tgg gat ccc atg att act aca 192
 48 Cys Glu Gly His Phe Ser Leu Ser Gln Trp Asp Pro Met Ile Thr Thr
 49 50 55 60
 51 tta cct ggc ttg tac ctg gtg tca gtt gga gtg gtc aaa cct gcc att 240
 52 Leu Pro Gly Leu Tyr Leu Val Ser Val Gly Val Val Lys Pro Ala Ile
 53 65 70 75 80
 55 tgg atc ttt gga tgg tct gaa cat gtt gtc tgc tcc att ggg atg ctc 288
 56 Trp Ile Phe Gly Trp Ser Glu His Val Val Cys Ser Ile Gly Met Leu
 57 85 90 95
 59 aga ttt gtt aat ctt ctc ttc agt gtt ggc aac ttc tat tta cta tat 336
 60 Arg Phe Val Asn Leu Leu Phe Ser Val Gly Asn Phe Tyr Leu Leu Tyr
 61 100 105 110
 63 ttg ctt ttc cac aag gta caa ccc aga aac aag gct gcc tca agt atc 384

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64	Leu	Leu	Phe	His	Lys	Val	Gln	Pro	Arg	Asn	Lys	Ala	Ala	Ser	Ser	Ile		
65	115						120					125						
67	cag	aga	gtc	ttg	tca	aca	tta	aca	cta	gca	gta	ttt	cca	aca	ctt	tat	432	
68	Gln	Arg	Val	Leu	Ser	Thr	Leu	Thr	Leu	Ala	Val	Phe	Pro	Thr	Leu	Tyr		
69	130						135					140						
71	ttt	ttt	aac	ttc	ctt	tat	tat	aca	gaa	gca	gga	tct	atg	ttt	ttt	act	480	
72	Phe	Phe	Asn	Phe	Leu	Tyr	Tyr	Thr	Glu	Ala	Gly	Ser	Met	Phe	Phe	Thr		
73	145						150				155		160					
75	ctt	ttt	gca	tat	ttg	atg	tgt	ctt	tat	gga	aat	cat	aaa	act	tca	gcc	528	
76	Leu	Phe	Ala	Tyr	Leu	Met	Cys	Leu	Tyr	Gly	Asn	His	Lys	Thr	Ser	Ala		
77	165						170					175						
79	ttc	ctt	gga	ttt	tgt	ggc	ttc	atg	ttt	cgg	caa	aca	aat	atc	atc	tgg	576	
80	Phe	Leu	Gly	Phe	Cys	Gly	Phe	Met	Phe	Arg	Gln	Thr	Asn	Ile	Ile	Trp		
81	180						185					190						
83	gct	gtc	tcc	tgt	gca	ggg	aat	gtc	att	gca	caa	aag	tta	act	gag	gct	624	
84	Ala	Val	Phe	Cys	Ala	Gly	Asn	Val	Ile	Ala	Gln	Lys	Leu	Thr	Glu	Ala		
85	195						200					205						
87	tgg	aaa	act	gag	cta	caa	aag	aag	gaa	gac	aga	ctt	cca	cct	att	aaa	672	
88	Trp	Lys	Thr	Glu	Leu	Gln	Lys	Lys	Glu	Asp	Arg	Leu	Pro	Pro	Ile	Lys		
89	210						215					220						
91	gga	cca	ttt	gca	gaa	ttc	aga	aaa	att	ctt	cag	ttt	ctt	ttg	gct	tat	720	
92	Gly	Pro	Phe	Ala	Glu	Phe	Arg	Lys	Ile	Leu	Gln	Phe	Leu	Leu	Ala	Tyr		
93	225						230				235		240					
95	tcc	atg	tcc	ttt	aaa	aac	ttg	agt	atg	ctt	ttc	tgt	ttg	act	tgg	ccc	768	
96	Ser	Met	Ser	Phe	Lys	Asn	Leu	Ser	Met	Leu	Phe	Cys	Leu	Thr	Trp	Pro		
97	245						250					255						
99	tac	atc	ctt	ctg	gga	ttt	ctg	ttt	tgt	gtc	ttt	gta	gta	gtt	aat	ggt	816	
100	Tyr	Ile	Leu	Leu	Gly	Phe	Leu	Phe	Cys	Ala	Phe	Val	Val	Val	Asn	Gly		
101	260						265					270						
103	gga	att	gtt	att	ggc	gat	cg	agg	atg	atg	cat	gaa	gcc	tgt	ctt	cat	ttt	864
104	Gly	Ile	Val	Ile	Gly	Asp	Arg	Ser	Ser	His	Glu	Ala	Cys	Leu	His	Phe		
105	275						280					285						
107	cct	caa	cta	tcc	tac	ttt	ttt	tca	ttt	act	ctc	ttt	ttt	tct	ttt	cct	912	
108	Pro	Gln	Leu	Phe	Tyr	Phe	Phe	Ser	Phe	Thr	Leu	Phe	Phe	Ser	Phe	Pro		
109	290						295					300						
111	cat	ctc	ctg	tct	cct	agg	aaa	att	aag	act	ttt	ctt	tcc	tta	gtt	tgg	960	
112	His	Leu	Leu	Ser	Pro	Ser	Lys	Ile	Lys	Thr	Phe	Leu	Ser	Leu	Val	Trp		
113	305						310				315		320					
115	aaa	cat	gga	att	ctg	ttt	ttg	gtg	gtt	acc	tta	gtc	tct	gtg	ttt	tta	1008	
116	Lys	His	Gly	Ile	Leu	Phe	Leu	Val	Val	Thr	Leu	Val	Ser	Val	Phe	Leu		
117	325						330					335						
119	gtt	tgg	aaa	ttc	act	tat	gtt	cat	aaa	tac	ttg	cta	gca	gac	aat	aga	1056	
120	Val	Trp	Lys	Phe	Thr	Tyr	Ala	His	Lys	Tyr	Leu	Leu	Ala	Asp	Asn	Arg		
121	340						345					350						
123	cat	tat	act	ttc	tat	gtg	tgg	aaa	aga	gtt	ttt	caa	aga	tat	gca	att	1104	
124	His	Tyr	Thr	Phe	Tyr	Val	Trp	Lys	Arg	Val	Phe	Gln	Arg	Tyr	Ala	Ile		
125	355						360					365						
127	ctg	aaa	tat	ttg	tta	gtt	cca	gcc	tat	ata	ttt	gct	gtt	tgg	agt	ata	1152	
128	Leu	Lys	Tyr	Leu	Leu	Val	Pro	Ala	Tyr	Ile	Phe	Ala	Gly	Trp	Ser	Ile		

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129	370	375	380	
131	gct gac tca ttg aaa tca aag cca att ttt tgg aat tta atg ttt ttc			1200
132	Ala Asp Ser Leu Lys Ser Lys Pro Ile Phe Trp Asn Leu Met Phe Phe			
133	385	390	395	400
135	ata tgc ttg ttc att gtt ata gtt cct cag aaa ctg ctg gaa ttt cgt			1248
136	Ile Cys Leu Phe Ile Val Ile Val Pro Gln Lys Leu Leu Glu Phe Arg			
137	405	410	415	
139	tac ttc att tta cct tat gtc att tat agg ctt aac ata act ctg cct			1296
140	Tyr Phe Ile Leu Pro Tyr Val Ile Tyr Arg Leu Asn Ile Thr Leu Pro			
141	420	425	430	
143	ccc aca tcc aga ctt gtt tgt gaa ctg agt tgc tat gca att gtt aat			1344
144	Pro Thr Ser Arg Leu Val Cys Glu Leu Ser Cys Tyr Ala Ile Val Asn			
145	435	440	445	
147	ttc ata act ttt tac atc ttt ctg aac aag act ttt cag tgg cca aat			1392
148	Phe Ile Thr Phe Tyr Ile Phe Leu Asn Lys Thr Phe Gln Trp Pro Asn			
149	450	455	460	
151	agt cag gac att caa agg ttt atg tgg taa tatcagtgtat attttgaact			1442
152	Ser Gln Asp Ile Gln Arg Phe Met Trp			
153	465	470		
W-->	155 gtaaaaatgg acttaataat agaccatttc tacaaaagaac aactgaatag gngaaaaaca			1502
157	tggaatttct ttaggtgcgttgcata tttagttttt taatatatat			1562
159	tttaaacata tgtaagaaat taagtggcaa agaactggga aagcttaaga cctgcttcaa			1622
W-->	161 angcctgaat aatggaaaaaa taaaanwngtt tncagatatac tcatacgct cnnknatgn			1682
W-->	163 tggcccytmn caangcttgg gaatgkttnn wntgnataag ttnattaaan ctgggnntgc			1742
W-->	165 tnnmwatnac ttnnnkncca nccwnnnwac natgnntan nnantattta caaaggcag			1802
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175	<220> FEATURE:			
176	<221> NAME/KEY: misc_feature			
177	<222> LOCATION: (1)..(1857)			
178	<223> OTHER INFORMATION: n is any nucleic acid			
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186	Phe Leu Val Ser Cys Leu Leu Phe Ser Ala Phe Ser Arg Ala Leu Arg			
187	20	25	30	
190	Glu Pro Tyr Met Asp Glu Ile Phe His Leu Pro Gln Ala Gln Arg Tyr			
191	35	40	45	
194	Cys Glu Gly His Phe Ser Leu Ser Gln Trp Asp Pro Met Ile Thr Thr			
195	50	55	60	
198	Leu Pro Gly Leu Tyr Leu Val Ser Val Gly Val Val Lys Pro Ala Ile			
199	65	70	75	80
202	Trp Ile Phe Gly Trp Ser Glu His Val Val Cys Ser Ile Gly Met Leu			
203	85	90	95	
206	Arg Phe Val Asn Leu Leu Phe Ser Val Gly Asn Phe Tyr Leu Leu Tyr			
207	100	105	110	

DV

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TIME: 09:42:25

Input Set : A:\HERG-KCR1rev1.ST25.txt
 Output Set: N:\CRF4\08122002\J000151B.raw

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210 Leu Leu Phe His Lys Val Gln Pro Arg Asn Lys Ala Ala Ser Ser Ile
211      115          120          125
214 Gln Arg Val Leu Ser Thr Leu Thr Leu Ala Val Phe Pro Thr Leu Tyr
215      130          135          140
218 Phe Phe Asn Phe Leu Tyr Tyr Glu Ala Gly Ser Met Phe Phe Thr
219      145          150          155          160
222 Leu Phe Ala Tyr Leu Met Cys Leu Tyr Gly Asn His Lys Thr Ser Ala
223      165          170          175
226 Phe Leu Gly Phe Cys Gly Phe Met Phe Arg Gln Thr Asn Ile Ile Trp
227      180          185          190
230 Ala Val Phe Cys Ala Gly Asn Val Ile Ala Gln Lys Leu Thr Glu Ala
231      195          200          205
234 Trp Lys Thr Glu Leu Gln Lys Lys Glu Asp Arg Leu Pro Pro Ile Lys
235      210          215          220
238 Gly Pro Phe Ala Glu Phe Arg Lys Ile Leu Gln Phe Leu Leu Ala Tyr
239      225          230          235          240
242 Ser Met Ser Phe Lys Asn Leu Ser Met Leu Phe Cys Leu Thr Trp Pro
243      245          250          255
246 Tyr Ile Leu Leu Gly Phe Leu Phe Cys Ala Phe Val Val Val Asn Gly
247      260          265          270
250 Gly Ile Val Ile Gly Asp Arg Ser Ser His Glu Ala Cys Leu His Phe
251      275          280          285
254 Pro Gln Leu Phe Tyr Phe Phe Ser Phe Thr Leu Phe Phe Ser Phe Pro
255      290          295          300
258 His Leu Leu Ser Pro Ser Lys Ile Lys Thr Phe Leu Ser Leu Val Trp
259      305          310          315          320
262 Lys His Gly Ile Leu Phe Leu Val Val Thr Leu Val Ser Val Phe Leu
263      325          330          335
266 Val Trp Lys Phe Thr Tyr Ala His Lys Tyr Leu Leu Ala Asp Asn Arg
267      340          345          350
270 His Tyr Thr Phe Tyr Val Trp Lys Arg Val Phe Gln Arg Tyr Ala Ile
271      355          360          365
274 Leu Lys Tyr Leu Leu Val Pro Ala Tyr Ile Phe Ala Gly Trp Ser Ile
275      370          375          380
278 Ala Asp Ser Leu Lys Ser Lys Pro Ile Phe Trp Asn Leu Met Phe Phe
279      385          390          395          400
282 Ile Cys Leu Phe Ile Val Ile Val Pro Gln Lys Leu Leu Glu Phe Arg
283      405          410          415
286 Tyr Phe Ile Leu Pro Tyr Val Ile Tyr Arg Leu Asn Ile Thr Leu Pro
287      420          425          430
290 Pro Thr Ser Arg Leu Val Cys Glu Leu Ser Cys Tyr Ala Ile Val Asn
291      435          440          445
294 Phe Ile Thr Phe Tyr Ile Phe Leu Asn Lys Thr Phe Gln Trp Pro Asn
295      450          455          460
298 Ser Gln Asp Ile Gln Arg Phe Met Trp
299      465          470
302 <210> SEQ ID NO: 3
303 <211> LENGTH: 1159
304 <212> TYPE: PRT

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RAW SEQUENCE LISTING
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Input Set : A:\HERG-KCR1rev1.ST25.txt
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305 <213> ORGANISM: Homo sapiens
 307 <400> SEQUENCE: 3
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 313 Thr Ile Ile Arg Lys Phe Glu Gly Gln Ser Arg Lys Phe Ile Ile Ala
 314 20 25 30
 317 Asn Ala Arg Val Glu Asn Cys Ala Val Ile Tyr Cys Asn Asp Gly Phe
 318 35 40 45
 321 Cys Glu Leu Cys Gly Tyr Ser Arg Ala Glu Val Met Gln Arg Pro Cys
 322 50 55 60
 325 Thr Cys Asp Phe Leu His Gly Pro Arg Thr Gln Arg Arg Ala Ala Ala
 326 65 70 75 80
 329 Gln Ile Ala Gln Ala Leu Leu Gly Ala Glu Glu Arg Lys Val Glu Ile
 330 85 90 95
 333 Ala Phe Tyr Arg Lys Asp Gly Ser Cys Phe Leu Cys Leu Val Asp Val
 334 100 105 110
 337 Val Pro Val Lys Asn Glu Asp Gly Ala Val Ile Met Phe Ile Leu Asn
 338 115 120 125
 341 Phe Glu Val Val Met Glu Lys Asp Met Val Gly Ser Pro Ala His Asp
 342 130 135 140
 345 Thr Asn His Arg Gly Pro Pro Thr Ser Trp Leu Ala Pro Gly Arg Ala
 346 145 150 155 160
 349 Lys Thr Phe Arg Leu Lys Leu Pro Ala Leu Leu Ala Leu Thr Ala Arg
 350 165 170 175
 353 Glu Ser Ser Val Arg Ser Gly Gly Ala Gly Gly Ala Gly Ala Pro Gly
 354 180 185 190
 357 Ala Val Val Val Asp Val Asp Leu Thr Pro Ala Ala Pro Ser Ser Glu
 358 195 200 205
 361 Ser Leu Ala Leu Asp Glu Val Thr Ala Met Asp Asn His Val Ala Gly
 362 210 215 220
 365 Leu Gly Pro Ala Glu Glu Arg Arg Ala Leu Val Gly Pro Gly Ser Pro
 366 225 230 235 240
 369 Pro Arg Ser Ala Pro Gly Gln Leu Pro Ser Pro Arg Ala His Ser Leu
 370 245 250 255
 373 Asn Pro Asp Ala Ser Gly Ser Ser Cys Ser Leu Ala Arg Thr Arg Ser
 374 260 265 270
 377 Arg Glu Ser Cys Ala Ser Val Arg Arg Ala Ser Ser Ala Asp Asp Ile
 378 275 280 285
 381 Glu Ala Met Arg Ala Gly Val Leu Pro Pro Pro Pro Arg His Ala Ser
 382 290 295 300
 385 Thr Gly Ala Met His Pro Leu Arg Ser Gly Leu Leu Asn Ser Thr Ser
 386 305 310 315 320
 389 Asp Ser Asp Leu Val Arg Tyr Arg Thr Ile Ser Lys Ile Pro Gln Ile
 390 325 330 335
 393 Thr Leu Asn Phe Val Asp Leu Lys Gly Asp Pro Phe Leu Ala Ser Pro
 394 340 345 350
 397 Thr Ser Asp Arg Glu Ile Ile Ala Pro Lys Ile Lys Glu Arg Thr His
 398 355 360 365
 401 Asn Val Thr Glu Lys Val Thr Gln Val Leu Ser Leu Gly Ala Asp Val

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 08/12/2002
PATENT APPLICATION: US/10/000,151B TIME: 09:42:26

Input Set : A:\HERG-KCR1rev1.ST25.txt
Output Set: N:\CRF4\08122002\J000151B.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 1494,1624,1647,1649,1654,1674,1675,1676,1678,1682,1692,1696
Seq#:1; N Pos. 1711,1712,1714,1717,1725,1732,1738,1739,1744,1745,1750,1755
Seq#:1; N Pos. 1756,1757,1759,1763,1767,1768,1769,1773,1777,1778,1779,1782
Seq#:1; N Pos. 1783,1784,1786,1830,1849,1853

VERIFICATION SUMMARY DATE: 08/12/2002
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Input Set : A:\HERG-KCRLrev1.ST25.txt
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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:155 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1442
L:161 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1622
L:163 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1682
L:165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1742
L:167 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1802